

SEQUENCE LISTING

<110> SIMMONS, ANTHONY
CHEN, JIANMIN

<120> COMPOSITIONS AND METHODS FOR HERPES SIMPLEX PROPHYLAXIS
AND TREATMENT

<130> UTFG:263WO

<140> UNKNOWN

<141> 2004-07-26

<150> 60/489,984

<151> 2003-07-23

<160> 36

<170> PatentIn Ver. 2.1

<210> 1

<211> 921

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 1

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gacatccaga tgacccagtc tccatcctcc ttatctgect ctctgggaga aagagtcagt 180
ctcacttgctc gggcaagtca ggaaattagt gcttacttaa gctggcttca gcagaaacca 240
gatggaacta ttaaacgcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 300
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttgagtct 360
gaagattttg cagactatta ctgtctacaa tatgctagtt atccgctcac gttcggtgct 420
gggaccaagc tggagctggg cgggtggcga tcgggtggag gaggcagcgg aggcggtggt 480
tcggtgaagc tgcaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 540
tcctgcaagg cttctggcta caccttcaca agctcctatg tacactgggt gaagcagagg 600
cctggacagg gacttgagtg gattggatgg atttatcctg gacatagtag tactaagtac 660
aatgagaagt tcatgggcaa gaccatattg actgcggaca aatcctccag cacagcctac 720
atgttgctca gcagcctgac ctctgaggac tctgcgatat atttctgtac aaggcaggag 780
gtacgactct ggtacttcga tgtctggggc gcagggacca cggtcaccgt ctccgcggcc 840
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<210> 2

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 2

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Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
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Lys Leu Gly Thr Glu Leu Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
 35 40 45
 Ser Ser Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg
 50 55 60
 Ala Ser Gln Glu Ile Ser Ala Tyr Leu Ser Trp Leu Gln Gln Lys Pro
 65 70 75 80
 Asp Gly Thr Ile Lys Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp Ser
 85 90 95
 Gly Val Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser
 100 105 110
 Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
 115 120 125
 Leu Gln Tyr Ala Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 130 135 140
 Glu Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160
 Ser Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 165 170 175
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
 180 185 190
 Tyr Val His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 195 200 205
 Gly Trp Ile Tyr Pro Gly His Ser Ser Thr Lys Tyr Asn Glu Lys Phe
 210 215 220
 Met Gly Lys Thr Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 225 230 235 240
 Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
 245 250 255
 Thr Arg Gln Glu Val Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala Gly
 260 265 270
 Thr Thr Val Thr Val Ser Ala Ala Ala Arg Gly Gly Pro Glu Gln Lys
 275 280 285
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 290 295 300
 His His
 305

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

Primer

<400> 3
tggtgggaag atggatacag 20

<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 4
ggtgatatcg tgatracmca rgatgaactc tc 32

<210> 5
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 5
ggtgatatcw tgmtgaccca awtccactc tc 32

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 6
ggtgatatcg tkctcacyca rtctccagca at 32

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
ctgwtgttct ggattcctg 19

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 8
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<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 9
tcagcttcyt gctaatacagt g 21

<210> 10
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<213> Artificial Sequence

<220>
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Primer

<400> 10
tgggtatctg gtrcstgtg 19

<210> 11
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<213> Artificial Sequence

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Primer

<400> 11
gtttcmaggt rccagatgt 19

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

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Primer

<400> 12
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<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13

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<210> 14

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14

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18

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15

taacccttga ccaggcatcc

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<210> 16

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 16

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36

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 17

aggvtmaact gcagvagtcw gg

22

<210> 18

<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 18
aggtvvagct gcagvagtcw gg 22

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 19
actgcaggtr tccactcc 18

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 20
rctacaggtg tccactcc 18

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 21
gcyacagmtg tccactcc 18

<210> 22
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 22
actgcaggtg tcctctct 18

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 23
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18

<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 24
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18

<210> 25
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 25
ccaagctgtg tcctrtcc

18

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 26
tgttgacagy cvttcckggt

20

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 27
taytttaaaa rgtgtcmagt gt

22

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 28
ctyttaaaag gkggtccagwg 20

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 29
cyttttamatg gstatccagtg t 21

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 30
atggcagcwg cycaaag 17

<210> 31
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 31
ctttttaaag wtgtccagkg t 21

<210> 32
<211> 19
<212> DNA
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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 32
cttcctgatg gcagtgggtt

19

<210> 33
<211> 904
<212> PRT
<213> human herpesvirus 1

<400> 33
Met Arg Gln Gly Ala Pro Ala Arg Gly Arg Arg Trp Phe Val Val Trp
1 5 10 15
Ala Leu Leu Gly Leu Thr Leu Gly Val Leu Val Ala Ser Ala Ala Pro
20 25 30
Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn
35 40 45
Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Ala Pro Pro Thr
50 55 60
Gly Asp Pro Lys Pro Lys Lys Asn Arg Lys Pro Lys Pro Pro Lys Pro
65 70 75 80
Pro Arg Pro Ala Gly Asp Asn Ala Thr Val Ala Ala Gly His Ala Thr
85 90 95
Leu Arg Glu His Leu Arg Asp Ile Lys Ala Glu Asn Thr Asp Ala Asn
100 105 110
Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu
115 120 125
Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu
130 135 140
Gly Ile Ala Val Val Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys
145 150 155 160
Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly
165 170 175
His Arg Tyr Ser Gln Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val
180 185 190
Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg
195 200 205
Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His
210 215 220
Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala
225 230 235 240
Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro
245 250 255
Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile
260 265 270
Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val
275 280 285

Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg
 290 295 300
 Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys
 305 310 315 320
 Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala
 325 330 335
 Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val
 340 345 350
 Ala Trp Asp Trp Val Pro Lys Arg Pro Ser Val Cys Thr Met Thr Lys
 355 360 365
 Trp Gln Glu Val Asp Glu Met Leu Arg Ser Glu Tyr Gly Gly Ser Phe
 370 375 380
 Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr
 385 390 395 400
 Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly Asp Cys Ile Gly Lys Asp
 405 410 415
 Ala Arg Asp Ala Met Asp Arg Ile Phe Ala Arg Arg Tyr Asn Ala Thr
 420 425 430
 His Ile Lys Val Gly Gln Pro Gln Tyr Tyr Leu Ala Asn Gly Gly Phe
 435 440 445
 Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr
 450 455 460
 Val Arg Glu His Leu Arg Glu Gln Ser Arg Lys Pro Pro Asn Pro Thr
 465 470 475 480
 Pro Pro Pro Pro Gly Ala Ser Ala Asn Ala Ser Val Glu Arg Ile Lys
 485 490 495
 Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His
 500 505 510
 Ile Gln Arg His Val Asn Asp Met Leu Gly Arg Val Ala Ile Ala Trp
 515 520 525
 Cys Glu Leu Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys
 530 535 540
 Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser
 545 550 555 560
 Ala Arg Met Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val
 565 570 575
 Ala Ala Asp Asn Val Ile Val Gln Asn Ser Met Arg Ile Ser Ser Arg
 580 585 590
 Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp
 595 600 605
 Gln Gly Pro Leu Val Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg
 610 615 620

Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr Val Gly His Arg Arg Tyr
 625 630 635 640
 Phe Thr Phe Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser
 645 650 655
 His Gln Leu Ser Arg Ala Asp Ile Thr Thr Val Ser Thr Phe Ile Asp
 660 665 670
 Leu Asn Ile Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val
 675 680 685
 Tyr Thr Arg His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu
 690 695 700
 Val Gln Arg Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp
 705 710 715 720
 Thr Val Ile His Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Gly
 725 730 735
 Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val
 740 745 750
 Val Met Gly Ile Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser
 755 760 765
 Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val
 770 775 780
 Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg
 785 790 795 800
 Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu
 805 810 815
 Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Glu Gly
 820 825 830
 Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
 835 840 845
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys
 850 855 860
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val
 865 870 875 880
 Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp
 885 890 895
 Gly Asp Ala Asp Glu Asp Asp Leu
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 <210> 34
 <211> 904
 <212> PRT
 <213> human herpesvirus 2
 <400> 34
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Ala Ala Val	Ala Ser Ala	Ala Pro Ala	Ala Pro Arg Ala
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Ser Gly Gly	Val Ala Ala	Thr Val Ala	Ala Asn Gly Gly
35		40	45
Arg Pro Pro	Pro Val Pro	Ser Pro Ala	Thr Thr Lys Ala
50		55	60
Lys Thr Lys	Lys Pro Pro	Lys Arg Pro	Glu Ala Thr Pro
65		70	75
Ala Asn Ala	Thr Val Ala	Ala Ala Gly	His Ala Thr Leu
	85		90
Arg Glu Ile	Lys Val Glu	Asn Ala Asp	Ala Gln Phe Tyr
	100		110
Pro Pro Thr	Gly Ala Thr	Val Val Gln	Phe Glu Gln Pro
	115		125
Pro Thr Arg	Pro Glu Gly	Gln Asn Tyr	Thr Glu Gly Ile
	130		140
Phe Lys Glu	Asn Ile Ala	Pro Tyr Lys	Phe Lys Ala Thr
145		150	155
Lys Asp Val	Thr Val Ser	Gln Val Trp	Phe Gly His Arg
	165		175
Phe Met Gly	Ile Phe Glu	Asp Arg Ala	Pro Val Pro Phe
	180		190
Ile Asp Lys	Ile Asn Thr	Lys Gly Val	Cys Arg Ser Thr
	195		205
Val Arg Asn	Asn Met Glu	Thr Thr Ala	Phe His Arg Asp
	210		220
Thr Asp Met	Glu Leu Lys	Pro Ala Lys	Val Ala Thr Arg
225		230	240
Gly Trp His	Thr Thr Asp	Leu Lys Tyr	Asn Pro Ser Arg
	245		255
Phe His Arg	Tyr Gly Thr	Thr Val Asn	Cys Ile Val Glu
	260		270
Ala Arg Ser	Val Tyr Pro	Tyr Asp Glu	Phe Val Leu Ala
	275		285
Phe Val Tyr	Met Ser Pro	Phe Tyr Gly	Tyr Arg Glu Gly
	290		300
Glu His Thr	Ser Tyr Ala	Ala Asp Arg	Phe Lys Gln Val
305		310	315
Tyr Ala Arg	Asp Leu Thr	Thr Lys Ala	Arg Ala Thr Ser
	325		335
Arg Asn Leu	Leu Thr Thr	Pro Lys Phe	Thr Val Ala Trp

340	345	350
Pro Lys Arg Pro Ala Val Cys Thr Met Thr Lys Trp Gln Glu Val Asp		
355	360	365
Glu Met Leu Arg Ala Glu Tyr Gly Gly Ser Phe Arg Phe Ser Ser Asp		
370	375	380
Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr Glu Tyr Ser Leu Ser		
385	390	395
Arg Val Asp Leu Gly Asp Cys Ile Gly Arg Asp Ala Arg Glu Ala Ile		
405	410	415
Asp Arg Met Phe Ala Arg Lys Tyr Asn Ala Thr His Ile Lys Val Gly		
420	425	430
Gln Pro Gln Tyr Tyr Leu Ala Thr Gly Gly Phe Leu Ile Ala Tyr Gln		
435	440	445
Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr Val Arg Glu Tyr Met		
450	455	460
Arg Glu Gln Asp Arg Lys Pro Arg Asn Ala Thr Pro Ala Pro Leu Arg		
465	470	475
Glu Ala Pro Ser Ala Asn Ala Ser Val Glu Arg Ile Lys Thr Thr Ser		
485	490	495
Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His Ile Gln Arg		
500	505	510
His Val Asn Asp Met Leu Gly Arg Ile Ala Val Ala Trp Cys Glu Leu		
515	520	525
Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys Leu Asn Pro		
530	535	540
Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser Ala Arg Met		
545	550	555
Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val Ala Pro Asp		
565	570	575
Asn Val Ile Val Gln Asn Ser Met Arg Val Ser Ser Arg Pro Gly Thr		
580	585	590
Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp Gln Gly Pro		
595	600	605
Leu Ile Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg Leu Thr Arg		
610	615	620
Asp Ala Leu Glu Pro Cys Thr Val Gly His Arg Arg Tyr Phe Ile Phe		
625	630	635
Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser His Gln Leu		
645	650	655
Ser Arg Ala Asp Val Thr Thr Val Ser Thr Phe Ile Asp Leu Asn Ile		
660	665	670
Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val Tyr Thr Arg		

675 680 685
 His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu Val Gln Arg
 690 695 700
 Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp Thr Val Ile
 705 710 715 720
 Arg Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Cys Ala Phe Phe
 725 730 735
 Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val Val Met Gly
 740 745 750
 Val Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser Ser Phe Met
 755 760 765
 Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val Leu Ala Gly
 770 775 780
 Leu Val Ala Ala Phe Phe Ala Phe Arg Tyr Val Leu Gln Leu Gln Arg
 785 790 795 800
 Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu Leu Lys Thr
 805 810 815
 Ser Asp Pro Gly Gly Val Gly Gly Glu Gly Glu Glu Gly Ala Glu Gly
 820 825 830
 Gly Gly Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
 835 840 845
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Arg
 850 855 860
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ser Lys Val Thr Asn Met Val
 865 870 875 880
 Leu Arg Lys Arg Asn Lys Ala Arg Tyr Ser Pro Leu His Asn Glu Asp
 885 890 895
 Glu Ala Gly Asp Glu Asp Glu Leu
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<210> 35

<211> 394

<212> PRT

<213> human herpesvirus 1

<400> 35

Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
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Ile Val Gly Leu His Gly Val Arg Ser Lys Tyr Ala Leu Val Asp Ala
 20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Arg Arg Val Tyr His
 50 55 60

Ile Gln Ala Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile
 65 70 75 80
 Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85 90 95
 Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp
 100 105 110
 Val Arg Lys Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly
 115 120 125
 Gly Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser
 130 135 140
 Tyr Asn Lys Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145 150 155 160
 Asn Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165 170 175
 Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180 185 190
 Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195 200 205
 Arg Ala Lys Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210 215 220
 Ser Ala Cys Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp
 225 230 235 240
 Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245 250 255
 Ala Val Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro
 260 265 270
 Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala
 275 280 285
 Thr Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290 295 300
 Glu Asp Pro Val Gly Thr Val Ala Pro Gln Ile Pro Pro Asn Trp His
 305 310 315 320
 Ile Pro Ser Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr
 325 330 335
 Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val Gly Gly Ser Leu Leu
 340 345 350
 Ala Ala Leu Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg His Thr
 355 360 365
 Gln Lys Ala Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp
 370 375 380
 Gln Pro Ser Ser His Gln Pro Leu Phe Tyr
 385 390

<210> 36

<211> 393

<212> PRT

<213> human herpesvirus 2

<400> 36

Met Gly Arg Leu Thr Ser Gly Val Gly Thr Ala Ala Leu Leu Val Val
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Ala Val Gly Leu Arg Val Val Cys Ala Lys Tyr Ala Leu Ala Asp Pro
 20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asn Leu Pro
 35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Lys Arg Val Tyr His
 50 55 60

Ile Gln Pro Ser Leu Glu Asp Pro Phe Gln Pro Pro Ser Ile Pro Ile
 65 70 75 80

Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85 90 95

His Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Asp Glu
 100 105 110

Ala Arg Lys His Thr Tyr Asn Leu Thr Ile Ala Trp Tyr Arg Met Gly
 115 120 125

Asp Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Pro
 130 135 140

Tyr Asn Lys Ser Leu Gly Val Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145 150 155 160

Ser Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165 170 175

Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180 185 190

Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195 200 205

Arg Ala Arg Ala Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210 215 220

Ala Ala Cys Leu Thr Ser Lys Ala Tyr Gln Gln Gly Val Thr Val Asp
 225 230 235 240

Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245 250 255

Ala Leu Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Pro Pro
 260 265 270

Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Asp Thr Thr Asn Ala
 275 280 285

Thr Gln Pro Glu Leu Val Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290 295 300

Glu Asp Pro Ala Gly Thr Val Ser Ser Gln Ile Pro Pro Asn Trp His
305 310 315 320

Ile Pro Ser Ile Gln Asp Val Ala Pro His His Ala Pro Ala Ala Pro
325 330 335

Ser Asn Pro Gly Leu Ile Ile Gly Ala Leu Ala Gly Ser Thr Leu Ala
340 345 350

Val Leu Val Ile Gly Gly Ile Ala Phe Trp Val Arg Arg Arg Ala Gln
355 360 365

Met Ala Pro Lys Arg Leu Arg Leu Pro His Ile Arg Asp Asp Asp Ala
370 375 380

Pro Pro Ser His Gln Pro Leu Phe Tyr
385 390